

Formate Final Insert

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Our Formate SDM1 VR Sequence

>FormateSDM1-VR_F02.ab1

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We used an NEB site directed mutagenesis kit to insert this stop codon into this sequence

BLAST of our Formate VR Sequence

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Query	2776	TTACTGTT	GCAGTGAAGT	GACTGGTAG	TAACGTTG	TGCTGTTGC	AGAGATGAG	TTGATGA	2835
Sbjct	996	TTACTGTT	GCAGTGAAGT	GACTGGTAG	TAACGTTG	TGCTGTTGC	AGAGATGAG	TTGATGA	937
Query	2836	GAATTTTG	ATTCTTATG	AGGAAC	TTTCGTTCC	TGGATATA	AACCAAGTTG	TGAAGGAGAGT	2895
Sbjct	936	GAATTTTG	ATTCTTATG	AGGAAC	TTTCGTTCC	TGGATATA	AACCAAGTTG	TGAAGGAGAGT	877
Query	2896	GGAAATGT	GGCAGGTAT	CGCTTAT	AGAGCATAC	GATCTTGA	AGGMAAAC	CATAGGTA	2955
Sbjct	876	GGAAATGT	GGCAGGTAT	CGCTTAT	AGAGCATAC	GATCTTGA	AGGMAAAC	CATAGGTA	817
Query	2956	TTGGAGCT	GGTAGAAT	TGGAAG	TTTACTTTT	GCAGAGGT	TGAAAC	CATTTGGT	3015
Sbjct	816	TTGGAGCT	GGTAGAAT	TGGAAG	TTTACTTTT	GCAGAGGT	TGAAAC	CATTTGGT	757
Query	3016	TCTTATAC	CATGATAG	GGCTCCAA	ATGGCTCC	TGAATTAG	AGAAGGMA	ACAGGTC	3075
Sbjct	756	TCTTATAC	CATGATAG	GGCTCCAA	ATGGCTCC	TGAATTAG	AGAAGGMA	ACAGGTC	697
Query	3076	TCGTTGAG	GATCTTAAT	GAGATG	TTGCCAA	AGTGC	GATGTTAT	AGTGATTA	3135
Sbjct	696	TCGTTGAG	GATCTTAAT	GAGATG	TTGCCAA	AGTGC	GATGTTAT	AGTGATTA	637
Query	3136	TCACAGAG	MAAACAG	AGGAATG	TTCAATA	AGGAACT	CATAGGMA	AATTAAG	3195
Sbjct	636	TCACAGAG	MAAACAG	AGGAATG	TTCAATA	AGGAACT	CATAGGMA	AATTAAG	577
Query	3196	TTTTGATC	GTGAATA	ACGCTAG	AGGAGCT	TATTATG	GMAAGGC	AGGCTGT	3255
Sbjct	576	TTTTGATC	GTGAATA	ACGCTAG	AGGAGCT	TATTATG	GMAAGGC	AGGCTGT	517
Query	3256	TTGMAATC	AGGACAC	ATCGGAG	GTATAGT	GAGATG	TTTGGG	ACCCTCA	3315
Sbjct	516	TTGMAATC	AGGACAC	ATCGGAG	GTATAGT	GAGATG	TTTGGG	ACCCTCA	457
Query	3316	AGGATCAT	CCATGG	AGATAC	ATGCC	TAAC	AGGCTAT	GACTCC	3375
Sbjct	456	AGGATCAT	CCATGG	AGATAC	ATGCC	TAAC	AGGCTAT	GACTCC	397
Query	3376	CAATCGAT	GTGCAACT	CAGATAT	GCAAGCT	GGAAC	TAAGGATAT	GTTAGAG	3435
Sbjct	396	CAATCGAT	GTGCAACT	CAGATAT	GCAAGCT	GGAAC	TAAGGATAT	GTTAGAG	337
Query	3436	AAGGTGA	AAGATTTT	CCAAC	CGAGAAT	TACATAG	TGAAGGAT	GGTGAAC	3495
Sbjct	336	AAGGTGA	AAGATTTT	CCAAC	CGAGAAT	TACATAG	TGAAGGAT	GGTGAAC	277
Query	3496	ACAGGTAA	TACTAG	AGCCAG	GCATCAA	ATAAA	CGAAAGG	CTCAGT	3555
Sbjct	276	ACAGGTAA	TACTAG	AGCCAG	GCATCAA	ATAAA	CGAAAGG	CTCAGT	217
Query	3556	TTTCGTTT	TATCTG	TTGTTT	GTGCGG	TGAACG	CTCTCT	ACTAGAGT	3615
Sbjct	216	TTTCGTTT	TATCTG	TTGTTT	GTGCGG	TGAACG	CTCTCT	ACTAGAGT	157
Query	3616	TCGGGTG	GGCCTTT	CTGCGT	TTTATA				3640
Sbjct	156	TCGGGTG	GGCCTTT	CTGCGT	TTTATA				132

Our Achieved Formate1 F Mid Sequence

>Formate1-Fmid_F10.ab1

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BLAST of our Formate F Mid Sequence

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Query 2269 TGTACCAGAAAGTGACCAGTGGAGAGATTGATCCTAGAGCTATAATTACTCACAAACTCC 2328
Sbjct 21 TGTACCAGAN-CTGACCAGTGGAGAGATTGATCCTAGAGCTATAATTACTCACAAACTCC 79

Query 2329 CATTAGATGAAGCTGCACACGCATACCATATCTTCAACGATAAACAGGATGATTGCATAA 2388
Sbjct 80 CATTAGATGAAGCTGCACACGCATACCATATCTTCAACGATAAACAGGATGATTGCATAA 139

Query 2389 AAGTGATTCTCAAGCCTTAATACTAGAGTCACACAGGAAAGTACTAGATGTCTTCAGGAG 2448
Sbjct 140 AAGTGATTCTCAAGCCTTAATACTAGAGTCACACAGGAAAGTACTAGATGTCTTCAGGAG 199

Query 2449 ATAGTAAGAAAATTGTTGGTGTGTTTATAAGGCTAACGAGTACGCAACTAAAAATCCAA 2508
Sbjct 200 ATAGTAAGAAAATTGTTGGTGTGTTTATAAGGCTAACGAGTACGCAACTAAAAATCCAA 259

Query 2509 ACTTCCTTGGATGTGTGGAGAATGCTCTTGGTATTAGAGATTGGTTGGAATCACAAAGGAC 2568
Sbjct 260 ACTTCCTTGGATGTGTGGAGAATGCTCTTGGTATTAGAGATTGGTTGGAATCACAAAGGAC 319

Query 2569 ATCAGTATATCGTTACAGATGATAAGGAGGCTCCAGATTGCGAACTTGAGAAACATATTC 2628
Sbjct 320 ATCAGTATATCGTTACAGATGATAAGGAGGCTCCAGATTGCGAACTTGAGAAACATATTC 379

Query 2629 CTGATCTCCACGTTTTAACTCTACACCATTTTCATCTGCTTACGTGACCGCAGAAAGGA 2688
Sbjct 380 CTGATCTCCACGTTTTAACTCTACACCATTTTCATCTGCTTACGTGACCGCAGAAAGGA 439

Query 2689 TTAAGAAAGCTAAGAACTTGAAACTTTTGCTCACCGCAGGAATCGGTTTACAGATCACATTG 2748
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Query 2749 ATCTTCAAGCTGCTGCTGCTGCTGGACTTACTGTTGCTGAAGTGACTGGTAGTAACGTTG 2808
Sbjct 500 ATCTTCAAGCTGCTGCTGCTGCTGGACTTACTGTTGCTGAAGTGACTGGTAGTAACGTTG 559

Query 2809 TGTCTGTTGACAGAGATGAGTTGATGAGAAATTTGATTCTTATGAGGAACTTCGTTCCCTG 2868
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Sbjct 680 ATCTTGAAGGAAAAACCATAGGTACTGTTGGAGCTGGTAGAATTOGAAAGTTACTTTTGC 739

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Sbjct 860 GCGATGTTATAGTGATTAAACATGCCTCTCACAGAGAAAACAGAGGAATGTTCAATAGG 918

Query 3169 AACTCATAGGAAAATTAAGAAAGGTGTTTGTATCGTGAATAACGCTAGAGGAGCTATTA 3228
Sbjct 919 AACTCATAGGAAAATTAAGAAAGGTGTTTGTATCGTGAATAACGCTAGAGNANCTATTA 978

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Sbjct 979 TGGAAAGGCAGGCTGTGTGTGATGCAGTTGAATCAGGACACATCGGAGGTTATAGTGA 1037

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Our Formate VF2 sequence

>Formate1-vf2_G07.ab1

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BLAST of our Formate VF Sequence

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Query	61	ATGCGCATCACACAGGAAAGAGGCCTATGACAAACACACAATCTGCTTTTTTCATGCCAT	120
Sbjct	160	ATGCGCATCACACAGGAAAGAGGCCTATGACAAACACACAATCTGCTTTTTTCATGCCAT	219
Query	121	CGGTGAATCTGTTTGGGGCTGGAAGCGTCAATGAGGTAGGCACGCGTCTGGCAGACCTGG	180
Sbjct	220	CGGTGAATCTGTTTGGGGCTGGAAGCGTCAATGAGGTAGGCACGCGTCTGGCAGACCTGG	279
Query	181	GTGTCAAAAAGGCATTATTAGTTACTGATGCAGGTTTACACGGATTGGGTCTTTCCGAAA	240
Sbjct	280	GTGTCAAAAAGGCATTATTAGTTACTGATGCAGGTTTACACGGATTGGGTCTTTCCGAAA	339
Query	241	AGATTTCAAGCATTATTTCGCGCAGCGGGCGTAGAAGTGTGATTTCGCCAAAGCAGAGC	300
Sbjct	340	AGATTTCAAGCATTATTTCGCGCAGCGGGCGTAGAAGTGTGATTTCGCCAAAGCAGAGC	399
Query	301	CTAATCCCACAGATAAAAATGTTGCAGAGGGCTTAGAGGCGTATAACCGGAAAACCTGTG	360
Sbjct	400	CTAATCCCACAGATAAAAATGTTGCAGAGGGCTTAGAGGCGTATAACCGGAAAACCTGTG	459
Query	361	ACTCCATTGTACGCTGGGTGGCGGTTCCCTCCCATGATGCGGGGAAAGCGATTGCTCTTG	420
Sbjct	460	ACTCCATTGTACGCTGGGTGGCGGTTCCCTCCCATGATGCGGGGAAAGCGATTGCTCTTG	519
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Sbjct	520	TTGCGGCTAACGGGGGTAAAGATTATGACTACGAAGGGGTAGACGTTTCGAAAGAGCCGA	579
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Sbjct	580	TGGTTCCCTTGATCGCGATCAATACCACTGCCGGAACGGGTAGCGAGCTGACAAAGTTCA	639
Query	541	CGATTATTACTGATACGGAACGCAAGTCAAAATGGCAATCGTAGATAAACATGTTACTC	600
Sbjct	640	CGATTATTACTGATACGGAACGCAAGTCAAAATGGCAATCGTAGATAAACNNGTTACTC	699
Query	601	CAACCCCTTCGATCAATGATCCAGAGCTTATGGTTGGGATGCCACCCTCGCTGACGGCCG	660
Sbjct	700	CAACCCCTTCGATCAATGATCCAGAGCTTATGGNTGGGATGCCACCCTCGCTGACGGCCG	759
Query	661	CGACTGGCTTGGACGCACTTACTCATGCGATCGAGGCATACGTTTCAACCGGGCGACTC	720
Sbjct	760	CGACTGGCTTGNACGCACTTACTCNTGCGATCGAGGCATACGTTTCAACCGGGCGACTC	819
Query	721	CTATCACTGACGCGTGGCAATCCAGGCGATCAAAATCATCAGTAAGTACTTACCACGTG	780
Sbjct	820	CTATCACTGACNCGTTGGCNATCCAGGCGATCAAAATCATCAGTAAGTACTTACCACGTG	879
Query	781	CTGTTGCGAATGGTAAAGACATTGAGGCCCGTGAA-CAAAATGGCGTTC	827
Sbjct	880	CTGTTGCNANNGNNAANACATTGAGGNCCGTGAACCNANTGGCGTTC	927

Fructose Final

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CAGTCGAAAGACTGGGCCTTTCTGTTTTATCTGTTGTTTGTCTGGTGAACGCTCTCTACTAGA
GTCACACTGGCTCACCTTCGGGTGGGCCTTTCTGCGTTTATA

Our Achieved Fructose VF2 Sequence

NNNNNNNNNNNNNNNNNACGACCGAGCGCAGCGAGTCAGTGAGCGAGGAAGCCTGCATAACGCG
AAGTAATCTTTTCGGTTTTAAAGAAAAAGGGCAGGGTGGTGACACCTTGCCCTTTTTTGCCGGA
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TCTAGTAGAGAGCGTTCACCGACAAACAACAGATAAAACGAAAGGCCAGTCTTTCGACTGAGC
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TGTCTGCTCAAATAAGGAGCCCATTTGGTTGAATCGTCTCGCGCGCTTCTGATTTATCTTTAGGG
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CAGCGGCAATAGTACCCCGATACTCTTAGCTTTCTGCGCCATACTTACAAGCGATTTTCGTTTC
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GGTAAGCATGCCGGCCTTTCCTGTGTGAAATATTTTATTACAACCCTTGCTTGACCAGTTTGTTA
ATCTTCTCAGCGGCTGCCTTCTTGTCGNNCTGANTAGCGATGCCACCCCTACAATGANCN

BLAST of Fructose

Query	1846	TCATTGTAGGGGGTGGCATCGCTAATCAGACCGACAAGAAGGCAGCCGCTGAGAAGATTA	1905
Sbjct	941	TCATTGTAGGGGGTGGCATCGCTANTCAGNCGACAAGAAGGCAGCCGCTGAGAAGATTA	882
Query	1906	ACAAACTGGTCAAGCAAGGGTTGTAATAAAATATTTACACAGGAAAGGCCGGCATGCTT	1965
Sbjct	881	ACAAACTGGTCAAGCAAGGGTTGTAATAAAATATTTACACAGGAAAGGCCGGCATGCTT	822
Query	1966	ACCACCGAGTTCTTAGCCGAAATCGTAAAGAGCTTAACAGCTCAGTTAATCAGATTGCG	2025
Sbjct	821	ACCACCGAGTTCTTAGCCGAAATCGTAAAGAGCTTAACAGCTCAGTTAATCAGATTGCG	762
Query	2026	GATGAGGAAGCAGAGGCACCTTGTTAATGGTATTTTCAGAGCAAAAAGTTTTCGTTGCC	2085
Sbjct	761	GATGAGGAAGCAGAGGCACCTTGTTAATGGTATTTTCAGAGCAAAAAGTTTTCGTTGCC	702
Query	2086	GGGGCTGGACGTTCTGGCTTCATGGCAAAGAGTTTTCGTATGCGTATGATGCATATGGGA	2145
Sbjct	701	GGGGCTGGACGTTCTGGCTTCATGGCAAAGAGTTTTCGTATGCGTATGATGCATATGGGA	642
Query	2146	ATCGACGCTTATGTAGTGGGAGAAACAGTTACCCGAATTACGAAAAAGAAGATATCCTT	2205
Sbjct	641	ATCGACGCTTATGTAGTGGGAGAAACAGTTACCCGAATTACGAAAAAGAAGATATCCTT	582
Query	2206	ATCATTGGATCGGGAAGTGGGGAACGAAATCGCTTGTAAGTATGGCGCAGAAAGCTAAG	2265
Sbjct	581	ATCATTGGATCGGGAAGTGGGGAACGAAATCGCTTGTAAGTATGGCGCAGAAAGCTAAG	522
Query	2266	AGTATCGGGGGTACTATTGCGCTGTACGATCAACCCAGAGTCTACGATTGGGCAATTA	2325
Sbjct	521	AGTATCGGGGGTACTATTGCGCTGTACGATCAACCCAGAGTCTACGATTGGGCAATTA	462
Query	2326	GCGGATATCGTCATTAAAAATGCCTGGGAGCCCTAAAGATAAATCAGAAGCGCGGAGACG	2385
Sbjct	461	GCGGATATCGTCATTAAAAATGCCTGGGAGCCCTAAAGATAAATCAGAAGCGCGGAGACG	402
Query	2386	ATTCAACCAATGGGCTCCTTATTTGAGCAGACATTATTATTGTTTTATGACGCCGTGATT	2445
Sbjct	401	ATTCAACCAATGGGCTCCTTATTTGAGCAGACATTATTATTGTTTTATGACGCCGTGATT	342
Query	2446	CTGCGCTTCATGGAAGAAGGGCTTAGATACGAAGACCATGTATGGCCGCCACGCAAAC	2505
Sbjct	341	CTGCGCTTCATGGAAGAAGGGCTTAGATACGAAGACCATGTATGGCCGCCACGCAAAC	282
Query	2506	CTTGAATAATAACTAGAGCCAGGCATCAAATAAAACGAAAGGCTCAGTCGAAAGACTG	2565
Sbjct	281	CTTGAATAATAACTAGAGCCAGGCATCAAATAAAACGAAAGGCTCAGTCGAAAGACTG	222
Query	2566	GGCCTTTCGTTTTATCTGTGTTTGTGCGGTGAACGCTCTCTACTAGAGTCACACTGGCTC	2625
Sbjct	221	GGCCTTTCGTTTTATCTGTGTTTGTGCGGTGAACGCTCTCTACTAGAGTCACACTGGCTC	162
Query	2626	ACCTTCGGGTGGGCCTTTCTGCGTTTATA	2654
Sbjct	161	ACCTTCGGGTGGGCCTTTCTGCGTTTATA	133

Our Achieved Fructose VR Sequence

>Fructosec32-vf2_A09.ab1

NNNNNNNNNNNTANCTANAAAATAGGCGTATCACGAGGCAGAATTTTCAGATAAAAAAATCCT
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GGCGTATAACGCGGAAAACGTGACTCCATTGTCACGCTGGGTGGCGGTTTCTCCCATGATGC
GGGGAAGCGATTGCTCTTGTTGCGGCTAACGGGGGTAAGATTCATGACTACGAAGGGGTAGA
CGTTTCGAAAGAGCCGATGGTTCCCTTGATCGCGATCAATACCACTGCCGGAACGGGTAGCGA
GCTGACAAAGTTCACGATTATTACTGATACGGAACGCAAAGTCAAATGGCAATCGTAGATAAA
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 CATGGNCTTTAACAACGCNNNTTAGGATACGTGCATGCAATCGCCCATCAGTTGGGGGGATTTT
 ACNATTTTCCGCATGGNNTGTGCAACGCTGNN

BLAST of our Fructose VR

Query	1	AAGCTTAATTGTGAGCGGATAACAATTGACATTGTGAGCGGATACAAAGATACTGAGCAC	60
Sbjct	100	AAGCTTAATTGTGAGCGGATAACAATTGACATTGTGAGCGGATACAAAGATACTGAGCAC	159
Query	61	ATACGTATCACACAGGAAGAGGCCCTATGACAAACACACAATCTGCTTTTTTCATGCCAT	120
Sbjct	160	ATACGTATCACACAGGAAGAGGCCCTATGACAAACACACAATCTGCTTTTTTCATGCCAT	219
Query	121	CGGTGAATCTGTTTGGGGCTGGAAGCGTCAATGAGGTAGGCACGCGTCTGGCAGACCTGG	180
Sbjct	220	CGGTGAATCTGTTTGGGGCTGGAAGCGTCAATGAGGTAGGCACGCGTCTGGCAGACCTGG	279
Query	181	GTGTCAAAAGGCATTATTAGTTACTGATGCAGGTTTACACGGATTGGGTCTTTCCGAAA	240
Sbjct	280	GTGTCAAAAGGCATTATTAGTTACTGATGCAGGTTTACACGGATTGGGTCTTTCCGAAA	339
Query	241	AGATTTCAAGCATTATTTCGCGCAGCGGGCGTAGAAGTGTGATTTTCCCAAAGCAGAGC	300
Sbjct	340	AGATTTCAAGCATTATTTCGCGCAGCGGGCGTAGAAGTGTGATTTTCCCAAAGCAGAGC	399
Query	301	CTAATCCCACAGATAAAAATGTTGCAGAGGGCTTAGAGGCGTATAACCGGAAAACGTG	360
Sbjct	400	CTAATCCCACAGATAAAAATGTTGCAGAGGGCTTAGAGGCGTATAACCGGAAAACGTG	459
Query	361	ACTCCATTGTGACGCTGGGTGGCGGTTCCCTCCCATGATGCGGGGAAGCGATTGCTCTTG	420
Sbjct	460	ACTCCATTGTGACGCTGGGTGGCGGTTCCCTCCCATGATGCGGGGAAGCGATTGCTCTTG	519
Query	421	TTGCGGCTAACGGGGGTAAAGTTTCATGACTACGAAGGGGTAGACGTTTCGAAAGAGCCGA	480
Sbjct	520	TTGCGGCTAACGGGGGTAAAGTTTCATGACTACGAAGGGGTAGACGTTTCGAAAGAGCCGA	579
Query	481	TGGTTCCCTTGATCGCGATCAATACCACCTGCCGGAACGGGTAGCGAGCTGACAAAGTTCA	540
Sbjct	580	TGGTTCCCTTGATCGCGATCAATACCACCTGCCGGAACGGGTAGCGAGCTGACAAAGTTCA	639
Query	541	CGATTATTACTGATACGGAAACGCAAGTCAAAATGGCAATCGTAGATAAACATGTTACTC	600
Sbjct	640	CGATTATTACTGATACGGAAACGCAAGTCAAAATGGCAATCGTAGATAAACATGTTACTC	699
Query	601	CAACCCCTTCGATCAATGATCCAGAGCTTATGGTTGGGATGCCACCCCTCGCTGACGGCCG	660
Sbjct	700	CAACCCCTTCGATCAATGATCCAGAGCTTATGGTTGGGATGCCACCCCTCGCTGACGGCCG	759
Query	661	CGACTGGCTTGGACGCACCTTACTCATGCGATCGAGGCATACGTTTCAACCGGGGCGACTC	720
Sbjct	760	CGACTGGCTTGGACGCACCTTACTCATGCGATCGAGGCATACGTTTCAACCGGGGCGACTC	819
Query	721	CTATCACTGACGCGTTGGCAATCCAGGCGATCAAAATCATCAGTAAGTACTTACCACGTG	780
Sbjct	820	CTATCACTGACGCGTTGGCAATCCAGGCGATCAAAATCATCAGTAAGTACTTACCACGTG	879
Query	781	CTGTTGCGAATGGTAAAGACATTGAGGCCCGTGAACAAATGGCGTTTCGCTCAATCACTTG	840
Sbjct	880	CTGTTGCGAATGGTAAAGACATTGAGGCCCGTGAACAAATGGCGTTTCGCTCAATCACTTG	939
Query	841	CTGGCATGGCCTTTAACAACGCAGGTTTAGGATACGTGCATGCAATCGCCCATCAGTTGG	900
Sbjct	940	CTGGCATGGNCTTTAACAACGCNNN-TTAGGATACGTGCATGCAATCGCCCATCAGTTGG	998
Query	901	GGGGATTTTACAAATTTTCCGCATGGAGTGTGCAACGCTG	939
Sbjct	999	GGGGATTTTACNAATTTTCCGCATGGNNTGTGCAACGCTG	1037

MDH2 with Lac insert

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 GTCAAAAAGGCATTATTAGTTACTGATGCAGGTTTACACGGATTGGGTCTTTCCGAAAAGAT
 TTCAAGCATTATTTCGCGCAGCGGGGCGTAGAAGTGTGATTTTCCCAAAGCAGAGCCTAAT
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TTGTCACGCTGGGTGGCGGTTCTCCCATGATGCGGGGAAAGCGATTGCTCTTGTTGCGG
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CGATCAATGATCCAGAGCTTATGGTTGGGATGCCACCCTCGCTGACGGCCGCGACTGGCT
TGGACGCACTTACTCATGCGATCGAGGCATACGTTTCAACCGGGGCGACTCCTATCACTGA
CGCGTTGGCAATCCAGGCGATCAAAATCATCAGTAAGTACTTACCACGTGCTGTTGCGAAT
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TTTAAACAACGCGAGGTTTAGGATACGTGCATGCAATCGCCCATCAGTTGGGGGGATTTTACA
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ACATCCCGAAGGGGTTCAAAGAACTGGGAGCCAAAGAGGAAGATATCGAGACTTTAGCCA
AGAACGCGATGAAGGATGCTTGTGCTCTGACAAACCCTCGCAAGCCCAAGTTGGAGGAGG
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Our Achieved MDH2 VR Sequence

>Mdh21reverse-VR_D06.ab1

NNNNNNNNNNNNNNNNNNNNNNNNNNNAGCGCAGCGAGTCAGTGAGCGAGGAAGCCTGCATAACGC
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T
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ATTTGTTACGGGCCTCAATGTCTTTACCATTGCAACAGCACGTGGTAAGTACTTACTGATGAT
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GATCGCATGAGTAAGTGCGTCCAAGCCAGTCGCGGCCGTCAGCGAGGGTGGCATCCCAACCA
TAAGCTCTGGATCATTGATCGAAAGGGTTGGAGTAACATGTTTATCTACGATTGCCATTTTGACT
TTGCGTTCCGTATCAGTAATAATCGTGAACTTTGTGAGCTCGCTACCCGTTCCGGCAGTGGTAT
TGATCGCGATCAAGGGAACCATCGGCTCTTTCGAAACGTCTACCCCTTCGTAGTCATGAATC

BLAST of our MDH2 VR Sequence

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Query 440 GATTCATGACTACGAAGGGGTAGACGTTTCGAAAGAGCCGATGGTTCCTTGATCGCGAT 499
Sbjct 933 GATTCATGACTACGAAGGGGTAGACGTTTCGAAAGAGCCGATGGTTCCTTGATCGCGAT 874
Query 500 CAATACCACTGCCGGAACGGGTAGCGAGCTGACAAAGTTCACGATTATTACTGATACGGA 559
Sbjct 873 CAATACCACTGCCGGAACGGGTAGCGAGCTGACAAAGTTCACGATTATTACTGATACGGA 814
Query 560 ACGCAAAGTCAAAATGGCAATCGTAGATAAACATGTTACTCCAACCCCTTTCGATCAATGA 619
Sbjct 813 ACGCAAAGTCAAAATGGCAATCGTAGATAAACATGTTACTCCAACCCCTTTCGATCAATGA 754
Query 620 TCCAGAGCTTATGGTTGGGATGCCACCCCTCGCTGACGGCCGCGACTGGCTTGGACGCACT 679
Sbjct 753 TCCAGAGCTTATGGTTGGGATGCCACCCCTCGCTGACGGCCGCGACTGGCTTGGACGCACT 694
Query 680 TACTCATGCGATCGAGGCATACGTTTCAACCGGGGCGACTCCTATCACTGACGCGTTGGC 739
Sbjct 693 TACTCATGCGATCGAGGCATACGTTTCAACCGGGGCGACTCCTATCACTGACGCGTTGGC 634
Query 740 AATCCAGGCGATCAAAATCATCAGTAAGTACTTACCACGTGCTGTTGCGAATGGTAAAGA 799
Sbjct 633 AATCCAGGCGATCAAAATCATCAGTAAGTACTTACCACGTGCTGTTGCGAATGGTAAAGA 574
Query 800 CATTGAGGCCCGTGAACAAATGGCGTTCGCTCAATCACTTGCTGGCATGGCCCTTAAACA 859
Sbjct 573 CATTGAGGCCCGTGAACAAATGGCGTTCGCTCAATCACTTGCTGGCATGGCCCTTAAACA 514
Query 860 CGCAGGTTTAGGATACGTGCATGCAATCGCCCATCAGTTGGGGGGATTTTACAATTTTCC 919
Sbjct 513 CGCAGGTTTAGGATACGTGCATGCAATCGCCCATCAGTTGGGGGGATTTTACAATTTTCC 454
Query 920 GCATGGAGTGTGCAACGCTGTACTTCTTCCCTACGTTTGTGCGCTTAAATTAATCTCTAA 979
Sbjct 453 GCATGGAGTGTGCAACGCTGTACTTCTTCCCTACGTTTGTGCGCTTAAATTAATCTCTAA 394
Query 980 AGTAGAACGCTATGCTGAAATCGCGCGCTTCTTGGGAGAAAACGTGGACGGCCTGAGTAC 1039
Sbjct 393 AGTAGAACGCTATGCTGAAATCGCGCGCTTCTTGGGAGAAAACGTGGACGGCCTGAGTAC 334
Query 1040 ATATGATGCTGCTGAGAAGGCCATTAAGGCTATCGAACGTATGGCCAAAGGATCTTAACAT 1099
Sbjct 333 ATATGATGCTGCTGAGAAGGCCATTAAGGCTATCGAACGTATGGCCAAAGGATCTTAACAT 274
Query 1100 CCCGAAGGGGTTCAAAGAAGTGGGAGCCAAAGAGGAAGATATCGAGACTTTAGCCAAGAA 1159
Sbjct 273 CCCGAAGGGGTTCAAAGAAGTGGGAGCCAAAGAGGAAGATATCGAGACTTTAGCCAAGAA 214
Query 1160 CGCGATGAAGGATGCTTGTGCTCTGACAAACCCCTCGCAAGCCCAAGTTGGAGGAGGTCAT 1219
Sbjct 213 CGCGATGAAGGATGCTTGTGCTCTGACAAACCCCTCGCAAGCCCAAGTTGGAGGAGGTCAT 154
Query 1220 TCAGATCATCAAAAACGCTATGTGATAATACTAG 1253
Sbjct 153 TCAGATCATCAAAAACGCTATGTGATAATACTAG 120

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Our Achieved MDH2 VF2 Sequence

>Mdh21-VF2_A06.ab1

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GNAGATGAAGTATCTNCNCGCCTGGGANNNCTGAGGGTATGTTNCGAGGAAGCAANGACGGN
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AAAATGAAAAGGATCTTTCACTACGCTAAAATCCTTTAAAAAAAACANNAGACCACATTTTTTAT
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BLAST of MDH2 VF2 Sequence

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Query 1 CACGTGAATTGTGAGCGGATAACAATTGACATTGTGAGCGGATAACAAGATACTGAGCAC 60
Sbjct 97 CACGTGAATTGTGAGCGGATAACAATTGACATTGTGAGCGGATAACAAGATACTGAGCAC 156
Query 61 ATGCGCATCACACAGGAAAGAGGCCATGACAAACACACAATCTGCTTTTTTCATGCCAT 120
Sbjct 157 ATGCGCATCACACAGGAAAGAGGCCATGACAAACACACAATCTGCTTTTTTCATGCCAT 216
Query 121 CGGTGAATCTGTTTGGGGCTGGA 143
Sbjct 217 CGGTGAATCTGTATGGTGNNTGGA 239

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MMOYZ Final

TCACACAGGAAAGTACTAGATGTCGATGCTGGGGGAGCGTCGTCGCGGATTAAGTACCC
 GGAAATGGCTGCTGTAATTTTGAAAGCCTTACCAGAGGCGCCACTGGATGGTAATAATAAG
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 TACGCCCAGCCTAATGCCGACTGGATCGCAGGTGGACTTGATTGGGGAGATTGGACCCAA
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 AGTCGAAAGACTGGGCCTTTTCGTTTTATCTGTTGTTTGTGCGGTGAACGCTCTCTACTACAGT
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Our MMOYZ Foward VF2 Sequence

>MMOYZ2forward-VF2_F06.ab1

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 TTAGCTTTTCGCTAAGGATGATTTCTGGAATTCGCGGCCGCTTCTAGAGTCACACAGGAAAGTAC
 TAGATGTCGATGCTGGGGGAGCGTCGTCGCGGATTAAGTACCCCGGAAATGGCTGCTGTAATT
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BLAST of our MMOYZ Forward VF2 Sequence

Query	1	TCACACAGGAAAGTACTAGATGTCGATGCTGGGGGAGCGTCGTCGCGGATTAACTGACCC	60
Sbjct	100	TCACACAGGAAAGTACTAGATGTCGATGCTGGGGGAGCGTCGTCGCGGATTAACTGACCC	159
Query	61	GGAAATGGCTGCTGTAATTTTGAAAGCCTTACCAGAGGCGCCACTGGATGGTAATAATAA	120
Sbjct	160	GGAAATGGCTGCTGTAATTTTGAAAGCCTTACCAGAGGCGCCACTGGATGGTAATAATAA	219
Query	121	GATGGGTACTTTGTAAACCCCGCGCTGGAAACGTTTGACCGAGTACGAGGCACTGACGGT	180
Sbjct	220	GATGGGTACTTTGTAAACCCCGCGCTGGAAACGTTTGACCGAGTACGAGGCACTGACGGT	279
Query	181	CTACGCCAGCCTAATGCCGACTGGATCGCAGGTGGACTTGATTGGGGAGATTGGACCCA	240
Sbjct	280	CTACGCCAGCCTAATGCCGACTGGATCGCAGGTGGACTTGATTGGGGAGATTGGACCCA	339
Query	241	AAAAATTCATGGCGGACGTCCTTCATGGGGTAATGAACCACAGAATTACGCACGGTTGA	300
Sbjct	340	AAAAATTCATGGCGGACGTCCTTCATGGGGTAATGAACCACAGAATTACGCACGGTTGA	399
Query	301	CTGGTTCAAGCATCGTGATCCACTGCGCCGTTGGCACGCGCCATATGTCAAGGACAAGGC	360
Sbjct	400	CTGGTTCAAGCATCGTGATCCACTGCGCCGTTGGCACGCGCCATATGTCAAGGACAAGGC	459
Query	361	AGAGGAATGGCGCTACACCGATCGCTTCCTTCAGGGCTATTACGCCGACGGTCAGATTCG	420
Sbjct	460	AGAGGAATGGCGCTACACCGATCGCTTCCTTCAGGGCTATTACGCCGACGGTCAGATTCG	519
Query	421	CGCGATGAATCCGACATGGCGCGACGAGTTTATCAATCGTTACTGGGGCGCCTTTTATTT	480
Sbjct	520	CGCGATGAATCCGACATGGCGCGACGAGTTTATCAATCGTTACTGGGGCGCCTTTTATTT	579
Query	481	CAATGAGTATGGTTTGTTTAACGCACATAGTCAGGGTGCCCGCGAGGCATTATCCGATGT	540
Sbjct	580	CAATGAGTATGGTTTGTTTAACGCACATAGTCAGGGTGCCCGCGAGGCATTATCCGATGT	639
Query	541	AACACGTGTAGTTTAGCATTTTGGGGTTTGTGATAAGATCGACATCGCCAGATGATCCA	600
Sbjct	640	AACACGTGTAGTTTAGCATTTTGGGGTTTGTGATAAGATCGACATCGCCAGATGATCCA	699
Query	601	ATTGGAGCGTGGGTTTCTGGCCAAAATTGTTCCAGGATTGACGAGTCCACGGCAGTGCC	660
Sbjct	700	ATTGGAGCGTGGGTTTCTGGCCAAAATTGTTCCAGGATTGACGAGTCCACGGCAGTGCC	759
Query	661	GAAGGCTGAATGGACGAACGGAGAAGTCTATAAATCTGCCCGTTAGCCGTTGAAGGACT	720
Sbjct	760	GAAGGCTGAATGGACGAACGGAGAAGTCTATAAATCTGCCCGTTAGCCGTTGAAGGACT	819
Query	721	GTGGCAGGAAGTGTTCGACTGGAACGAATCCGCGTTCTCGGTTACGCAGTTTACGACGC	780
Sbjct	820	GTGGCAGGAAGTGTTCGACTGGAACGAATCCGCGTTCTCGGTTACGCAGTTTACGACGC	879
Query	781	ATTGTTCCGGACAGTTCGTACGCCGCGAATTTTTCCAACGTCTGG	824
Sbjct	880	ATTGTTCCGGNCAGTTCGTACGCCGCGAATTTTTCCAACGTCTGG	923

Our MMOYZ Reverse VR Sequence

>MMOYZ2reverse-VR_H06.ab1

NNNNNNNNNNNNNNNNNNNNNANGANNNNNNNCGAGTCAGTGAGCGAGGAAGCCTGCATAACG
CGAAGTAATCTTTTCGGTTTTAAAGAAAAAGGGCAGGGTGGTGACACCTTGCCCTTTTTTGCC
GGACTGCAGCGGCCGCTACTAGTATATAAACGCAGAAAGGCCACCCGAAGGTGAGCCAGT
GTGACTGTAGTAGAGAGCGTTCACCGACAAACAACAGATAAAACGAAAGGCCAGTCTTTCG
ACTGAGCCTTTTCGTTTTATTTGATGCCTGGCTCTAGTATCAGGGGCTCTGCAGGTGAACAACG
CGCACTCCACGTTGCTTGCGTAACTCCTCCAGAGGCGTATCATAGTAATTCAGATTGCGTAAC
TCCATTAAGCGTGTTCCAAGTTGGCGCTCACCGTCTAAGAAGTAGTTCAGTGGCATGATAGGT
GGCTTGTATGCCTGGCGGAAGCCGATGTGGATTTTCTCCGCCTCCCACTTATCTTTCGCAGCA
TTCATTTTCGCTACAGTACCGTCTAATACGGATTTTCGCGTCTTCACCAAAGCTGTCTTGTGAC
GGAAATCTACTTCGTTGAACGCACGGGCTTTCAGGACTGCTACTTTCTCTTCCAGCTTAGCCT
CGATCCACAGGTAGTCGTTATCCAACCTCATAGCTATTGCGAAACGGGGTGGTGTGATCCATG
CGGAACTGCTTAAGCATCTCGGCAGCTTTTTCAAGCGTGTTTAATTGCGCAATTTTATTGACC
CACGCATCACGAGTGTCATTACTGTGGATGCCAATTTAGCCATCTAGTACTTTCCTGTGTGA
CTGTAGTATCACTTAAGGCCCGCTAAGACAGCCTTAACGATTTGGTCGCGGTCGGCTTTAAAA
TCAATACGGGAAGCGTAGTCCTCAATCCAGTC

BLAST of our MMOYZ Reverse VR Sequence

Query	1103	GACTGGATTGAGGACTACGCTTCCCGTATTGATTTTAAAGCCGACCGCGACCAATCGTT	1162
Sbjct	889	GACTGGATTGAGGACTACGCTTCCCGTATTGATTTTAAAGCCGACCGCGACCAATCGTT	830
Query	1163	AAGGCTGTCTTAGCGGGCCTTAAGTGATACTACAGTCACACAGGAAGTACTAGATGGCT	1222
Sbjct	829	AAGGCTGTCTTAGCGGGCCTTAAGTGATACTACAGTCACACAGGAAGTACTAGATGGCT	770
Query	1223	AAATTGGGCATCCACAGTAATGACACTCGTGATGCGTGGGTCAATAAAATTGCGCAATTA	1282
Sbjct	769	AAATTGGGCATCCACAGTAATGACACTCGTGATGCGTGGGTCAATAAAATTGCGCAATTA	710
Query	1283	AACACGCTTGAAAAGCTGCCGAGATGCTTAAGCAGTTCCGCATGGATCACCACCCCG	1342
Sbjct	709	AACACGCTTGAAAAGCTGCCGAGATGCTTAAGCAGTTCCGCATGGATCACCACCCCG	650
Query	1343	TTTCGCAATAGCTATGAGTTGGATAACGACTACCTGTGGATCGAGGCTAAGCTGGAAAGAG	1402
Sbjct	649	TTTCGCAATAGCTATGAGTTGGATAACGACTACCTGTGGATCGAGGCTAAGCTGGAAAGAG	590
Query	1403	AAAGTAGCAGTCCTGAAAGCCCGTGCGTTCAACGAAGTAGATTTCGGTCACAAGACAGCT	1462
Sbjct	589	AAAGTAGCAGTCCTGAAAGCCCGTGCGTTCAACGAAGTAGATTTCGGTCACAAGACAGCT	530
Query	1463	TTTGGTGAAGACCGCAATCCGTATTAGACGGTACTGTAGCGAAATGAATGCTGCGAAA	1522
Sbjct	529	TTTGGTGAAGACCGCAATCCGTATTAGACGGTACTGTAGCGAAATGAATGCTGCGAAA	470
Query	1523	GATAAGTGGGAGGCGGAGAAAATCCACATCGGCTTCCGCCAGGCATACAGCCACCTATC	1582
Sbjct	469	GATAAGTGGGAGGCGGAGAAAATCCACATCGGCTTCCGCCAGGCATACAGCCACCTATC	410
Query	1583	ATGCCAGTGAAGTACTTCTTAGACGGTGAGCGCCAACTTGGAAACAGCTTAATGGAGTTA	1642
Sbjct	409	ATGCCAGTGAAGTACTTCTTAGACGGTGAGCGCCAACTTGGAAACAGCTTAATGGAGTTA	350
Query	1643	CGCAATCTGAATTACTATGATACGCCCTCTGGAGGAGTTACGCAAGCAACGTGGAGTGCGC	1702
Sbjct	349	CGCAATCTGAATTACTATGATACGCCCTCTGGAGGAGTTACGCAAGCAACGTGGAGTGCGC	290
Query	1703	GTTGTTACCTGCAGAGCCCTGATACTAGAGCCAGGCATCAATAAAACGAAAGGCTCA	1762
Sbjct	289	GTTGTTACCTGCAGAGCCCTGATACTAGAGCCAGGCATCAATAAAACGAAAGGCTCA	230
Query	1763	GTCGAAAGACTGGGCCTTTTCGTTTATCTGTGTTTGTGCGGTGAACGCTCTCTACTACAG	1822
Sbjct	229	GTCGAAAGACTGGGCCTTTTCGTTTATCTGTGTTTGTGCGGTGAACGCTCTCTACTACAG	170
Query	1823	TCACACTGGCTCACCTTCGGGTGGGCCTTTCTGCGTTTATA	1863
Sbjct	169	TCACACTGGCTCACCTTCGGGTGGGCCTTTCTGCGTTTATA	129

RFP Fructose Final Insert

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 GGTTTCCCGACTGGAAAGCGGGCAGTGAGCGCAACGCAATTAATGTGAGTTAGCTCACTC
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 CGGATAACAATTTACACATACTAGAGAAAGAGGAGAAATACTAGATGGCTTCCTCCGAAG
 ACGTTATCAAAGAGTTCATGCGTTTCAAAGTTCGTATGGAAGGTTCCGTAAACGGTCACGA
 GTTCGAAATCGAAGGTGAAGGTGAAGGTCGTCCGTACGAAGGTACCCAGACCGCTAAACT
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 GTACGGTTCCAAAGCTTACGTTAAACACCCGGCTGACATCCCGGACTACCTGAAACTGTCC
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 CAACTTCCCGTCCGACGGTCCGTTATGCAGAAAAAAACCATGGGTGGGAAGCTTCCAC
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 AGCTGCCGGGTGCTTACAAAACCGACATCAAACCTGGACATCACCTCCCACAACGAAGACTA
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AAACCTTGAATAATAATACTAGAGCCAGGCATCAAATAAAACGAAAGGCTCAGTCGAAAGA
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CACCTTCGGGTGGGCCTTTCTGCGTTTATA

Our Achieved Fructose with RFP VF2 Sequence

>Fructosec3rfp1-VF2_C10.ab1

NNNNNNNNNNNNNANNTATNAAATAGGCGTATCACGAGGCAGAATTTTCAGATAAAAAAATC
CTTAGCTTTTCGCTAAGGATGATTTCTGGAATTCGCGGCCGCTTCTAGAGCAATACGCAAAC
CGCCTCTCCCCGCGCGTGGCCGATTCATTAATGCAGCTGGCACGACAGGTTTCCCGACT
GGAAAGCGGGCAGTGAGCGCAACGCAATTAATGTGAGTTAGCTCACTCATTAGGCACC
CCAGGCTTTACACTTTATGCTTCCGGCTCGTATGTTGTGTGGAATTGTGAGCGGATAACAA
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TCCTCCCTGCAAGACGGTGAGTTCATCTACAAAGTTAAACTGCGTGGTACCAACTTCCCGT
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TGCTTACAAAACCGACATCAAACTGGACATCACCTCCCACAACGAAGACTACACCATCGTT
GANAGTACGAACGTGCTGANNNCGTCACTCCACCGGNGCTTNATAACGCTGATANNGCTA
NTGNANNTCGN

BLAST of our RFP + Fructose VF2

Query	1	CAATACGCAAAACCGCCTCTCCCGCGCGTTGGCCGATTCAATTAATGCAGCTGGCACGACA	60
Sbjct	99	CAATACGCAAAACCGCCTCTCCCGCGCGTTGGCCGATTCAATTAATGCAGCTGGCACGACA	158
Query	61	GGTTTCCCGACTGGAAAGCGGGCAGTGAGCGCAACGCAATTAATGTGAGTTAGCTCACTC	120
Sbjct	159	GGTTTCCCGACTGGAAAGCGGGCAGTGAGCGCAACGCAATTAATGTGAGTTAGCTCACTC	218
Query	121	ATTAGGCACCCAGGCTTTACACTTTATGCTTCGGGCTCGTATGTTGTGTGGAATTGTGA	180
Sbjct	219	ATTAGGCACCCAGGCTTTACACTTTATGCTTCGGGCTCGTATGTTGTGTGGAATTGTGA	278
Query	181	GCGGATAACAATTTACACATACTAGAGAAAGAGGAGAAATACTAGATGGCTTCCTCCGA	240
Sbjct	279	GCGGATAACAATTTACACATACTAGAGAAAGAGGAGAAATACTAGATGGCTTCCTCCGA	338
Query	241	AGACGTTATCAAAAGAGTTTATGCGTTTCAAAGTTCGTATGGAAGGTTCCGTTAACGGTCA	300
Sbjct	339	AGACGTTATCAAAAGAGTTTATGCGTTTCAAAGTTCGTATGGAAGGTTCCGTTAACGGTCA	398
Query	301	CGAGTTTCGAAATCGAAGGTGAAGGTGAAGGTTCGTCGTCGTAACGAGGTACCCAGACCGCTAA	360
Sbjct	399	CGAGTTTCGAAATCGAAGGTGAAGGTGAAGGTTCGTCGTCGTAACGAGGTACCCAGACCGCTAA	458
Query	361	ACTGAAAGTTACCAAAGGTGGTCCGCTGCCGTTTCGCTTGGGACATCCTGTCCCGCAGTT	420
Sbjct	459	ACTGAAAGTTACCAAAGGTGGTCCGCTGCCGTTTCGCTTGGGACATCCTGTCCCGCAGTT	518
Query	421	CCAGTACGGTTCCCAAAGCTTACGTTAAACACCCGGCTGACATCCCGGACTACCTGAAACT	480
Sbjct	519	CCAGTACGGTTCCCAAAGCTTACGTTAAACACCCGGCTGACATCCCGGACTACCTGAAACT	578
Query	481	GTCTTCCCGGAAGGTTTCAAATGGGAACGTGTTATGAACCTCGAAGACGGTGGTGTGT	540
Sbjct	579	GTCTTCCCGGAAGGTTTCAAATGGGAACGTGTTATGAACCTCGAAGACGGTGGTGTGT	638
Query	541	TACCGTTACCCAGGACTCTCTCCCTGCAAGACGGTGAGTTTATCTACAAAGTTAAACTGCG	600
Sbjct	639	TACCGTTACCCAGGACTCTCTCCCTGCAAGACGGTGAGTTTATCTACAAAGTTAAACTGCG	698
Query	601	TGGTACCAACTTCCCGTCCGACGGTCCCGTTATGCAGAAAAAACCATGGGTGGGAAGC	660
Sbjct	699	TGGTACCAACTTCCCGTCCGACGGTCCCGTTATGCAGAAAAAACCATGGGTGGGAAGC	758
Query	661	TTCCACCGAACGTATGTACCCGGAAGACGGTGCTCTGAAAGGTGAAATCAAAATGCGTCT	720
Sbjct	759	TTCCACCGAACGTATGTACCCGGAAGACGGTGCTCTGAAAGGTGAAATCAAAATGCGTCT	818
Query	721	GAAACTGAAAGACGGTGGTCACTACGACGCTGAAGTTAAACACCTACATGGCTAAAAA	780
Sbjct	819	GAAACTGAAAGACGGTGGTCACTACGACGCTGAAGTTAAACACCTACATGGCTAAAAA	878
Query	781	GCCGGTTACAGTGCCGGGTGCTTACAAAACCGACATCAAACTGGACATCACCTCCACAA	840
Sbjct	879	ACCGGTTACAGTGCCGGGTGCTTACAAAACCGACATCAAACTGGACATCACCTCCACAA	938
Query	841	CGAAGACTACACCATCGTTGAACAGTACGAACGTGCTGAAGGTCGTCACTCCACCGGCGC	900
Sbjct	939	CGAAGACTACACCATCGTTGAN-AGTACGAACGTGCTGANNN-CGTCACTCCACCGGNGC	996
Query	901	TTAATAACGCTGATAGTGTAGTG 924	
Sbjct	997	TTNATAACGCTGATANNGCTANTG 1020	

Our Achieved Sequence of Fructose with RFP VR Sequence

>Fructosec3rfp1-VR_D10.ab1

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CGAAGTAATCTTTTCGGTTTTAAAGAAAAAGGGCAGGGTGGTGACACCTTGCCCTTTTTTGCCG
GACTGCAGCGGCCGCTACTAGTATATAAACGCAGAAAGGCCACCCGAAGGTGAGCCAGTGTG
ACTCTAGTAGAGAGCGTTACCCGACAAACAACAGATAAAACGAAAGGCCAGTCTTTCGACTGA
GCCTTTCGTTTTATTTGATGCCTGGCTCTAGTATTATTATTCAAGGTTTGGTGGCGGCCATACA
TGGTCTTCGTATCTAAGCCCTTCTTTTCCATGAAGCGCAGAATCACGGCGTCATAAAACAATAAT
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GCTCCCAGGCATTTTAATGACGATATCCGCTAATTGCCCAATCGTAGACTCTGGGTGATCGTG
ACAGCGGCAATAGTACCCCCGATACTCTTAGCTTTCTGCGCCATACTTACAAGCGATTTTCGTTT
CCCCACTTCCCGATCCAATGATAAGGATATCTTCTTTTCGTAATTCGGGGTAACTGTTTCTCC

CACTACATAAGCGTCGATTCCCATATGCATCATACGCATAGCAAAACTCTTTGCCATGAAGCCA
 GAACGTCCAGCCCCGGCAACGAAAACCTTTTTTGTCTGCAAAATACCATTAACAAGTGCCTCTG
 CTTCTCATCCGCAATCTGATTAAGTCTGTTAAGCTCTTTTACGATTTGGCTAAGAAGTCTG
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 TAATCTTCTCAGCGGCTGCCTTCTTGTCTGGTCTGATTAGCGATGCCACCCCTACAATGACC
 NAGTCAGGTTTACGCTTGATANNTCTGGGTAAAGTCTCTAACTTGNTTCCACCGGCGATGGCTG
 TCTTGGNNTTCTTCACNN

BLAST of our RFP Fructose VR Sequence

Query	2841	GTGAAGAACGCCAAGACAGCCATCGCCGGTGGAAATCAAGTTAGAGACTTTACC-AGAGGT	2899
Sbjct	1026	GTGAAGAAANNCCAAAGACAGCCATCGCCGGTGGAAATCAAGTTAGAGACTTTACCCAGA-NN	968
Query	2900	TATCAAGGCTGAACCTGACTTGGTCATTGTAGGGGGTGGCATCGCTAATCAGACCGACAA	2959
Sbjct	967	TATCAAGGCTGAACCTGACTTGGTCATTGTAGGGGGTGGCATCGCTAATCAGACCGACAA	908
Query	2960	GAAGGCAGCCGCTGAGAAGATTAAACAACTGGTCAAGCAAGGGTTGTAATAAAATATTTC	3019
Sbjct	907	GAAGGCAGCCGCTGAGAAGATTAAACAACTGGTCAAGCAAGGGTTGTAATAAAATATTTC	848
Query	3020	ACACAGGAAAGGCCCGGCATGCTTACCACCGAGTTCTTAGCCGAAATCGTAAAGAGCTTA	3079
Sbjct	847	ACACAGGAAAGGCCCGGCATGCTTACCACCGAGTTCTTAGCCGAAATCGTAAAGAGCTTA	788
Query	3080	ACAGCTCAGTTAATCAGATTGCGGATGAGGAAGCAGAGGCACTTGTAAATGGTATTTTGC	3139
Sbjct	787	ACAGCTCAGTTAATCAGATTGCGGATGAGGAAGCAGAGGCACTTGTAAATGGTATTTTGC	728
Query	3140	AGAGCAAAAAGTTTTTCGTTGCCGGGGCTGGACGTTCTGGCTTCATGGCAAGAGTTTTG	3199
Sbjct	727	AGAGCAAAAAGTTTTTCGTTGCCGGGGCTGGACGTTCTGGCTTCATGGCAAGAGTTTTG	668
Query	3200	CTATGCGTATGATGCATATGGGAATCGACGCTTATGTAGTGGGAGAAACAGTTACCCCGA	3259
Sbjct	667	CTATGCGTATGATGCATATGGGAATCGACGCTTATGTAGTGGGAGAAACAGTTACCCCGA	608
Query	3260	ATTACGAAAAGAGATATCCTTATCATGGATCGGGAAAGTGGGAAACGAAATCGCTTG	3319
Sbjct	607	ATTACGAAAAGAGATATCCTTATCATGGATCGGGAAAGTGGGAAACGAAATCGCTTG	548
Query	3320	TAAGTATGGCGCAGAAAGCTAAGAGTATCGGGGGTACTATTGCCGCTGTCACGATCAACC	3379
Sbjct	547	TAAGTATGGCGCAGAAAGCTAAGAGTATCGGGGGTACTATTGCCGCTGTCACGATCAACC	488
Query	3380	CAGAGTCTACGATTGGGCAATTAGCGGATATCGTCATTAAATGCCTGGGAGCCCTAAAG	3439
Sbjct	487	CAGAGTCTACGATTGGGCAATTAGCGGATATCGTCATTAAATGCCTGGGAGCCCTAAAG	428
Query	3440	ATAAATCAGAAAGCGCGGAGACGATTCAACCAATGGGCTCCTTATTTGAGCAGACATTAT	3499
Sbjct	427	ATAAATCAGAAAGCGCGGAGACGATTCAACCAATGGGCTCCTTATTTGAGCAGACATTAT	368
Query	3500	TATTGTTTTATGACGCCGTGATTCTGCGCTTCATGGAAAGAAGGGCTTAGATACGAAGA	3559
Sbjct	367	TATTGTTTTATGACGCCGTGATTCTGCGCTTCATGGAAAGAAGGGCTTAGATACGAAGA	308
Query	3560	CCATGTATGGCCGCCACGCAACCTTGAATAATACTAGAGCCAGGCATCAAAATAAAA	3619
Sbjct	307	CCATGTATGGCCGCCACGCAACCTTGAATAATACTAGAGCCAGGCATCAAAATAAAA	248
Query	3620	CGAAAGGCTCAGTCGAAAGACTGGGCCTTTTCGTTTTATCTGTTGTTTGTCTGGTGAACGCT	3679
Sbjct	247	CGAAAGGCTCAGTCGAAAGACTGGGCCTTTTCGTTTTATCTGTTGTTTGTCTGGTGAACGCT	188
Query	3680	CTCTACTAGAGTCACACTGGCTCACCTTCGGGTGGGCCTTTCTGCGTTTATA	3731
Sbjct	187	CTCTACTAGAGTCACACTGGCTCACCTTCGGGTGGGCCTTTCTGCGTTTATA	136